

Fig. 1

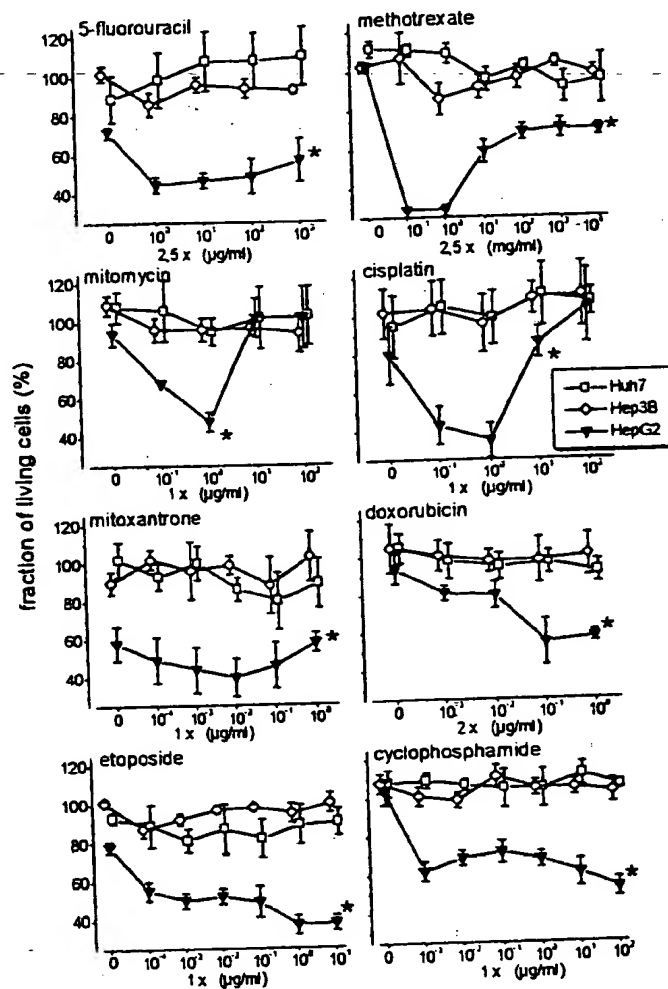


Fig. 2

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	532	24.1

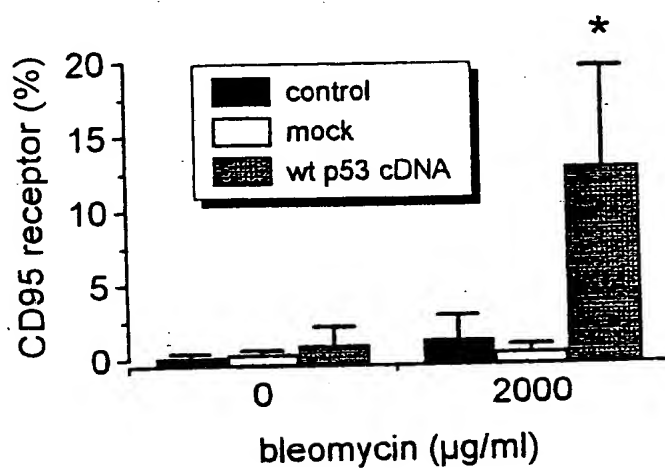


Fig. 3

APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	241

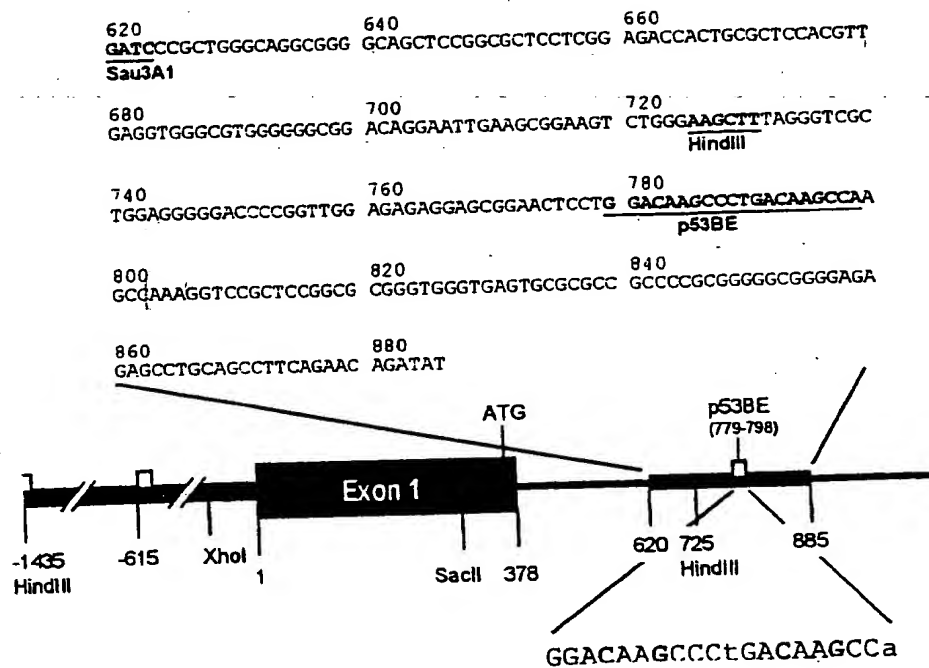


Fig. 4

TO2T40-1624E860

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	536 24.1

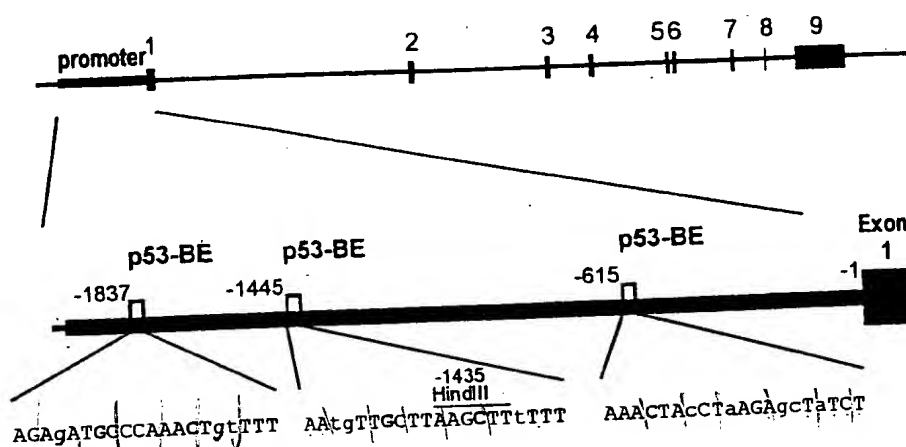


Fig. 5

0003491-04301

APPROVED	O G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	536 24.1

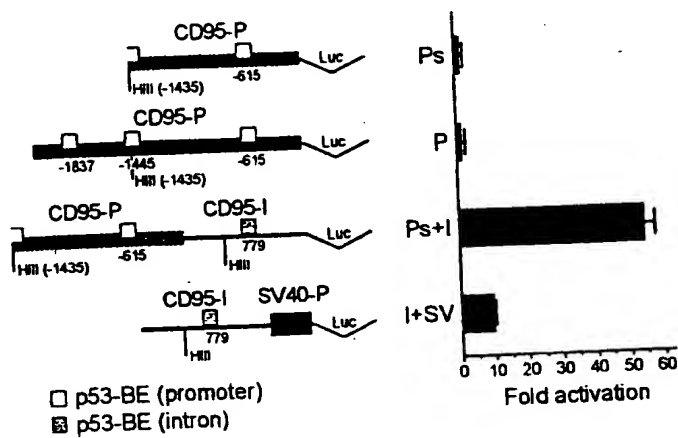


Fig. 6

APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

1 GATCCCCTGGGCGGGGCGGGGAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT 60  
 CTAGGGCGACCCGTCGCCCCGTCGAGGCGCGAGGAGCCTCTGGTGACGCGAGGTGCAA  
 61 GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC 120  
 CTCACCCGACCCCCCGCCTGTCTTAACCTTCGCCTTCAGACCCTTCGAAATCCAGCG  
 <---- 4.P53-BE ---->  
 (intron)  
 121 TGGAGGGGGACCCCGTTGGAGAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAAGCCAA 180  
 ACCTCCCCCTGGGGCCAACTCTCTCTCGCCTTGAGGACCTGTTGCGGACTGTTGCGTT  
 181 GCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGCGGGGAGA 240  
 CGGTTTCCAGGCGAGGCCCGCGCCACCCACTCACGCGCGCGGGGCGCCCCCGCCCTCT  
 241 GAGCCTACAGCCTTCAGAACACATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAA 300  
 CTCGGATGTCGGAAGTCTTGTGTATAACGAGTAAAGACCGTCAAGAGTCTGCATCCTTT  
 301 TAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTT 360  
 ATTCAAGTCGTGGCTTCGTCAACAATTCGGCCTCCCGAGCCTTCTTGCCGTGGAAAAGAAA  
 361 CTCGAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATT 420  
 GAGCTTTTCAATATACCCCCGACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAA  
 421 GTCACACAGAAAAGGAACTGCCTTGCTCCCTTCGGGAATTCTCTTTAAGACTGTA 480  
 CAGTGTGTCTTTTCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATCTGACAT  
 481 AGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTTCTGCCCTTCTTTCTTTCTTTG 540  
 TCAGCGACGGACTCACCAAAGTAAACAAAACAAAAGACGGGAAGAGAAAGAGAAAAC  
 541 CCCTTTCTTAGCTTGCACTCCCATGGTGATTCTGCTTGGTCTCCTGCTGGGGTTGGTGG 600  
 GGGAAAGAATCGAACGTGAGGGTACCACTAAAGACGAACGAGGACGACCCCAACCACC  
 601 TACTCGTTCCACCGCACAGAACCGGGCGCTATTATTGGCCAAGAACTTGAGCAGCCT 660  
 ATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAACTCGTCGGA  
 661 GTTTTGAAGTCCCTCGCTCAGAAATGCCAGCTTGCAAGTGGCTAATCAAGAGACGTG 720  
 CAAAACTTTTAGGGAGCGAGTCTTTACGGTCAACGTCTACCGATTAGTTTCTCTGCAC

Fig. 7

FOI b7D - 16242860





1091 TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGT 1140  
 AATTACACAATAATTACCCAACCTTAGATTAACCCCTTCCCTCTCTCCAACGTCTCACTCCA  
 GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA 1200  
 1141 CGTCTCGAACCACCTGCTACGGTTTCCTTATGACTTTGGAAATCACACAGGTCAGACCTT 1260  
 CTGCATCCAAATTCAGGTTTCACTAATGATGTCTTATCCAAACATACCTTCTGTAAAATT  
 1201 GACGTAGGTTTAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA 1260

←--- 3.p53-B2 ---→  
 (promoter)

1261 CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT 1320  
 GTACGATTGATGGATTCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTTGTCA  
 TCACCAGAGCACGAAGAATTACAAGATTTTTTTTTAAAGAAAATTGGCCAGGAAATAAT 1380  
 1321 AGTGGTCTCGTGCTTTCTTAATGTTCTAAAAAAAATTCTTTTAACCGGTCCTTTATTA  
 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGGCTATGCGATTG 1440  
 1381 CTCATTGCTTCTGTCTTCATTAACACTTACAAATTATATCGACCCGATACGCTAAAC  
 GCTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAAACTAAGGGGCCCTCCCTTTT 1500  
 1441 CGAATTCAACAATCGAAACAAAGGAGAACTCTTTATTTTGTATCCCCGGGAGGGA  
 CAGAGCCCTATGGCGCAACATCTGTACTTTTTTCATATGGTTAACTGTCCATTCCAGGAAC 1560  
 1501 GTCTCGGGATACCGCTGTAGACATGAAAAGTATACCAATTGACAGGTAAGGTCCTTG  
 GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCAGTCAAATGCCCCGCAAG 1620  
 1561 CAGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCCGGTCAGTTTACGGGGCGTTC  
 TCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC 1680  
 1621 AGAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCTGGAGACG  
 GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCCAGGTTGAACTACAGCAGAA 1740  
 1681 CGAGACTCGAGGTAAGAGGAAGTCTGGAGGGGTTGAAGGGTCCAACCTGATGTCGTCTT  
 GCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGC 1800  
 1741 CGGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTGC  
 CACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCTGACTCCTTCC 1860  
 1801 GTGACGTCCTTGCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGG  
 TCACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC 1920  
 1861 AGTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGGTTCAACGACTTAGTTACCTCG

Fig. 8B

T02T40 T624E860

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

1921 CCTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCCTCTGACCACCGGGGC 1980  
 GGAGGGGTTGGGCCCCGCAAGGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG  
 1981 TTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT 2040  
 AAAAGCACTCGAGCAGAGACTAGAGCGGTTCTCACTGTGTGTCCACAAGTTTCTGCGAA  
 2041 CTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTG 2100  
 GACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCGCCCGTGAC  
 2101 GCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTCTTCTCCCGC 2160  
 CGTGCTTGTGTGGGACTCCGGTCCGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCG  
 2161 GGACATGTACAGAGCTCGAGAGTACTAGTGGCCACGTGGGCGGTGCACCTTAAGCTTTA 2220  
 CCTGTACATGTCTCGAGCTCTTCATGATACCGGTGCACCCGGCACGTGGAATTCGAAT  
 ←---4.p53-BE-  
 (intron)  
 2221 GGGTCGCTGGAGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAGCCCTGAC 2280  
 CCCAGCGACCTCCCCCTGGGGCCACCTCTCTCCTCGCCTTGAGGACCTGTTCGGGACTG  
 -----→  
 2281 AAGCCAAGCCAAAGSTCCGCTCCGGCGCGGGTGGGTGAGTGC CGCGCCCGCGGGGGC 2340  
 TTCGGTTCGGTTTCCAGGCGAGGCCGCGCCACCCACTCACGCGCGGGGCGCCCCG  
 2341 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATGCTCATTTTCTGGCAGTTCCTCAGACG 2400  
 CCCCTCTCTCGGACGTCCGAAGTCTTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC  
 2401 TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT 2460  
 ATCCTTTATTCACTCGTGGCTTCGTCACCAATTCCGGCCTCCCGAGCCTTCTTGCCGTGGA  
 2461 TTTCTTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT 2520  
 AAAGAAAGAGCTTTTCAATATACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA  
 2521 TTTTATTGTCACACAGAAAAGGAACTGCCTTGTCTCCCTTCCGGAATTCTCTCTTAA 2580  
 AAAATAACAGTGTGTCTTTTCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAAT  
 2581 GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTGTTTTGTTTTTCTGCCCTTCTCTTTCT 2640  
 CTGACATTGAGCGGACTCACCAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA  
 2641 TCTTTTGCCTTTCTTAGCTTGCACTCCCATGGTGATTCTGCTTGGTCTCCTGCTGGGG 2700  
 AGAAAACGGGAAGAATCGAACGTGAGGGTACCCTAAAGACGAACAGAGGACGACCCC

Fig. 8C

10240" 1624E850

APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

2701 TTGGTGGTACTCGTTCCACCCGACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA  
 -----+-----+-----+-----+-----+ 2760  
 AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCGGGATAATAACCGGTTCTTTGAAC  
  
 2761 GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG  
 -----+-----+-----+-----+-----+ 2820  
 CGTCGGACAAAACCTTTTCAGGGAGCGAGTCTTTACGGTCGAACGCTCTACCGATTAGTTTC  
  
 2821 AGACGTG  
 ----- 2827  
 TCTGCAC

FO2F40" T624E860

Fig. 8D

APPROVED	O G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	536 24.1

<---- 1.p53-BE --

1 TGAGGACTCTCAGGAATATGCTGGTAAAATAAAAAATAACCTTTAGAGATGCCCAAACCTGT  
 60  
 ACTCCTGAGAGTCCTTATACGACCATTTTATTTTATTGGAAATCTCTACGGGTTTGACA

-->

61 TTCCCCCAGAACACCAGCATTTCATTAGGTGTTTCATTCAATAGATTCTTCAAAGGATTCCA  
 120  
 AAAGGGGTCTTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCCTAAGGT

121 AAGGCAAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCTTTGACATTAGCATAC  
 180  
 TTCCGTTTCTTCAAACCCCTTGTATATATTAATGGGTGGGAAACTGTAATCGTATG

181 TAAGGGCCCTGAGAAGTTTGGATTAGAAAGTTTCAAATTAAGTAACCCAGAATTTT  
 240  
 ATTCCCGGGACTCTTCAAACCTAATTCCTTTCAAAGTTTAAATTCATTGGGTCTTAAAA

241 CTAAGATTATTTGACCATGAACATATGCTCCCCACAAAGCACATATTCCTATCTCCTT  
 300  
 GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA

301 GAACTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA  
 360  
 CTTGAACTCCTATTAATCTGCATGCACCCATCTCCCATCCCCTTCCCCCATACCGTATCT

361 AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAAATTCCTGACTCTGCTATTTATTA  
 420  
 TTCTCGTCTGGAACCCCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT

<---- 2.p53-BE ---->

421 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTATTGTAAAG  
 480  
 TGATTGGTAGAAACGGTTACAACGAATTCGAAAAAACCGATGAAAAAATAAACATTTT

481 TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC  
 540  
 ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTCAATTCATTCTTCTAG

541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT  
 600  
 GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA

601 CCTTTCCCTTTTTTCTCTCTTCCCTCCTTCCATTCTTCTTCCCTTACCTCTCCTTTC  
 660  
 GGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAAGGAAGAAGGAATGGAGAGGAAG

Fig. 9A

T02T40-T624E860



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

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1561 GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCAGTCAAATGCCCCGCAAG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      CAGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCGGGTCACTTTACGGGGCGTTC
1621 TCTTTCTCTGAGTGAATCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      AGAAAGAGACTCACTGAGGTGTTAATCGGTTCCGAGGACATGGGTCCGTCCTGGAGACG
1681 GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCCAGGTTGAATACAGCAGAA
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      CGAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGGTCCAACCTGATGTCGTCTT
1741 GCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAATGAGCATGCCAGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      CGGAAATCTTTCCGCTCTCCGCGCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCG
1801 CACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCCTGACTCCTTCC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      GTGACGTCCTTGCGGGGCCCTGTCTTACGGGTAACACGTTGCTTGGGACTGAGGAAGG
1861 TCACCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      AGTGGGACTGAAGAGGGGGAGGGATGGGCGCGCGTCCGGTTCAACGACTTAGTTACCTCG
1921 CCTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCTTCCCATCTCTGACCACCGGGGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      GGAGGGGTTGGGCGCCGAAGGGTCCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG
1981 TTTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      AAAAGCACTCGAGCAGAGACTAGAGCGGTTCTCACTGTGTGTCCACAAGTTTCTGCGAA
2041 CTGGGGAGTGAGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGCGGGGCACTG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      GACCCCTCACTCCCTTCGCCAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCGTGAC
2101 GCACGGAACACACCCTGAGGCCAGCCCTGGCTGCCAGGGCGGAGCTGCCTCTTCTCCCGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      CGTGCCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCG
2161 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTTA
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      CCTGTACATGTCTCGAGCTCTTCATGATACCCGGTGACCCGGCACGTGGAATTCGAAT
      <---- 4.p53-BE
      (intron)
2221 GGGTCGCTGGAGGGGGACCCCGTTGGAGAGAGGAGCGGAATCCTGGACAAGCCCTGAC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      CCCAGCGACCTCCCTGGGGCCAACCTCTCTCCTCGCCTTGAGGACCTGTTCCGGGACTG
      ----->
2281 AAGCCAAGCCAAAGGTCCGCTCCGCGCGGGTGGGTGAGTGCCGCCGCCCGCGGGGGG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      TTCGGTTCGGTTTCCAGGGCAGGCGCGCCACCCACTCACGCGCGGCGGGGCGCCCCG
2341 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTTCTGGCAGTTCTCAGACG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
      CCCCTCTCTCGGACGTGGAAGTCTTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC

```

Fig. 9C

FOOTNOTES 1624E860

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

2401 TAGGAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT  
 -----+-----+-----+-----+-----+ 2460  
 ATCCTTTATTTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGA  
  
 2461 TTCTTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTTCTGGAGGCTTGTTCACGTT  
 -----+-----+-----+-----+-----+ 2520  
 AAAGAAGAGCTTTTCAATATACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA  
  
 2521 TTTTATTGTCACACAGAAAAGGAAACTGCCTTGCTCCCTCCGGGAATTCTCTCTTTAA  
 -----+-----+-----+-----+-----+ 2580  
 AAAATAACAGTGTGTCCTTTTCCTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAAT  
  
 2581 GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTTCTGCCCTTCTCTTTCT  
 -----+-----+-----+-----+-----+ 2640  
 CTGACATTCAGCGACGGACTCACCAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA  
  
 2641 TCTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGAATTCTGCTTGGTCTCCTGCTGGG  
 -----+-----+-----+-----+-----+ 2700  
 AGAAAACGGGAAAGAATCGAACGTGAGGGTACCACTAAGACGAACCAAGAGGACGACCCC  
  
 2701 TTGGTGGTACTCGTTCCCAACGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA  
 -----+-----+-----+-----+-----+ 2760  
 AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAAC  
  
 2761 GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGAGATGGCTAATCAAAG  
 -----+-----+-----+-----+-----+ 2820  
 CGTCGGACAAAACTTTTAGGGAGCGAGTCTTTACGGTCGAACGCTTACCGATTAGTTTC  
  
 2821 AGACGTG  
 ----- 2827  
 TCTGCAC

00034291 041204

Fig. 9D

<---- 1.p53-BE ---->  
(promoter)

1 TGAGGACTCTCAGGAATATGCTGGTAAATATAAATAACCTTTAGAGATGCCCAAACCTGT  
ACTCCTGAGAGTCCTTATACGACCATTTTATTTTATTGGAATCTCTACGGGTTTGACA 60

-->

61 TTTCCCAAGAACACCAGCATTCTAGGTGTTTCATTCAATAGATTCTTCAAAGGATTCCA  
AAAGGGGTCTTGTTGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCTTAAGGT 120  
AAGGCAAAGAAGTTTGGGGAACAGTATATATAATTACCCCAACCTTTGACATTAGCATAC  
121 TTCCGTTTCTTCAAACCCCTTGTCATATATATTAATGGGTGGGAACTGTAATCGTATG  
TAAGGGCCCTGAGAAGTTTGGGATTAAGAAAGTTTCAAATTAAAGTAACCCAGAATTTT 180  
181 ATTCCCGGACTCTTCAAACCTAATTCTTTCAAAGTTTAAATTTTCATTGGGTCTTAAAA  
CTAAGATTATTTGACCATGAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT 240  
241 GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA  
GAAGTTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA 300  
301 CTTGAACCTCTATTAATCTGCATGCACCATCTCCCATCCCCTTCCCCATACCGTATCT  
AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAAATTCCTGACTCTGCTATTTATTA 360  
361 TTCTCGTCTGGAACCCCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT 420

<---- 2.p53-BE ---->  
(promoter)

421 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTATTTGTAAAG  
TGATTGGTAGAAACGGTTACCAACGAATTCGAAAAAACCGATGTAATAAATAAACATTTT 480  
TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540  
481 ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTCTAATTCTCCTTCTAG  
CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGTACTGATTTTGTCAATTGT 600  
541 GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA  
CCTTTCCCTTTTTTTCTCTCTCCCTCCTTCCATTCTCTTCCCTTACCTCTCCTTTC 660  
601 GGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAAGGAAGAAGGAATGGAGAGGAAG  
CTTCCCTCACACCCCTTTTCTTCTCTTTTACATTTTTTTATTTAAATGAACTTTTC 720  
661 GAAGGGAGTGTGGGGAAGGAAGGAAGAAATGTAAAAAATAAATTTACTTGAAAG  
ATTTTGAATAGTTTGTAGGATTTCAAAAAATTTGCAGAGATAATACAGAGAATGCCATA 780  
721 TAAACCTTATCAAAATCTAAAGTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

Fig. 10A

0083491.041201



APPROVED	O G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS
	536 24.1

781 TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA 840  
 ATGGTAGGAGGAATAGGGTGAAGAAAAACAGATAATCTACGAGTCTCACACACGTGT  
 841 GGCTGGCAGCCCAGGGTCTTCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG 900  
 CCGACCGTGC GGGTCCAGAGGAGTACCGTGATTGTCTAGATGACTTTCCACCTTGTCTC  
 901 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG 960  
 TGTTCGGATAGTTGTGGATGTTCTGACCACCATTACGTCAGTGTCTACGTTTTGTGTCC  
 961 GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAACAGGCTCCAG 1020  
 CACTACCTTTCGGGAGTCTCTCCATTGGATTGGATCTAACTCCCGGGTTGTCCGAGGTC  
 1021 AAGAAAATGTCAACTGAGAGGAAGCCCTGAAGGATGAACAGTGGGCTAAGCAAAGGTTAT 1080  
 TTCTTTTACAGTTGACTCTCCTTCGGACTTCTACTTGTCAACCGATTGTTTCCCAATA  
 1081 TAATGTGTTATTAAATGGGTTGAATCTAATTGGGAAGGAGAGAGGTTGCAGAGTGAGGTG 1140  
 ATTACACAATAATTACCCAACTTAGATTAAACCTTCCCTCTCTCAACGTCTCACTCCAC  
 1141 CAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAAC 1200  
 GTCTCGAACCACCTGCTACGGTTTCCTTATGACTTTGGAAATCACACAGGTCAGACCTTG  
 1201 TGCATCCAAATTCAAGTTCAAGTAATGATGTCATTATCCAAACATACCTTCTGTAAATTC 1260  
 ACGTAGGTTTAAGTCCAAGTCATTACTACGTAATAGGTTTGTATGGAAGACATTTTAAG  
  
 <---- 3.p53-BE ---->  
 (promoter)  
 1261 ATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT 1320  
 TACGATTGTGATGGATTCTCGATAGATGGCAAGGTTTCGTATCACTGAAACTTGTACAA  
 1321 CACCAGAGCAGCAAGAAGATTACAAGATTTTTTTTAAAGAAAATTGGCCAGGAATAATG 1380  
 GTGGTCTCGTGCTTCTTAAATGTTCTAAAAAAAATTCTTTTAACCGGTCCTTTATTAC  
 1381 AGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAAATATAGCTGGGGCTATGCGATTGG 1440  
 TCATTGCTTCTGTCTTCATTAACACTTACAAATTATATCGACCCGATACGCTAAACC  
 1441 CTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAACTAAGGGGCCCTCCCTTTTC 1500  
 GAATTCAACAATCGAAACAAAGGAGAATCTTTATTTTGTATTCCCGGGAGGGAAG  
 1501 AGAGCCTTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCCAGAAACG 1560  
 TCTCGGAATACCGCGTTGTAGACATGAAAAGTATACCAATTGACAGGTAAGGTCTTTGC  
 1561 TCTGTAGCCTCTCATGTTGCAGCCACAACATGGACAGCCAGTCAATGCCCGCAAGT 1620  
 AGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCTGGGTCACTTTACGGGGGCTTCA  
 1621 CTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGCG 1680  
 GAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCCTGGAGACGC  
 1681 CTCTGAGCTCCATTCTCCTCAAGACCTCCCCAATTTCCAGGTTGAACTACAGCAGAAG 1740  
 GAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTGAAGGTTCAACTTGATGTCGTCTTC

Fig. 10B

09834291.041304

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

000424-041201

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1741 CCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCTCACCTGAAGTGAGCATGCCAGCC 1800
      +-----+-----+-----+-----+-----+
      GGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGACTTCACTCGTACGGTCGG

1801 ACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTGCAACGAACCTGACTCCTTCCT 1860
      +-----+-----+-----+-----+-----+
      TGACGTCTTGCGGGGCCCTGTCCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGGA

1861 CACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGCC 1920
      +-----+-----+-----+-----+-----+
      GTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGGTTCAACGACTTAGTTACCTCGG

1921 CTCCCCAACC CGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCTCTGACCACCGGGGCT 1980
      +-----+-----+-----+-----+-----+
      GAGGGGTTGGGCCCGCAAGGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCGA

1981 TTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTC 2040
      +-----+-----+-----+-----+-----+
      AAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGCCACAAGTTTCTGCGAAG

2041 TGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGG 2100
      +-----+-----+-----+-----+-----+
      ACCCCTCACTCCCTTCGCCAATGCTCACTGAACCGACCTCGGAGTCCCCGCGGTGACC

2101 CACGGAACACACCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCTCTTCTCCCGCG 2160
      +-----+-----+-----+-----+-----+
      GTGCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCGC

2161 GGTGTGGTGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTTCACCTTCGGAGGATTGCTCA 2220
      +-----+-----+-----+-----+-----+
      CCAACCACCTGGGCGAGTCATGCCTCAACCCCTTCGAGAAAGTGAAGCCTCCTAACGAGT

2221 ACAACCATGCTGGGCATCTGGACCTCCTACCTCTGGTGATCCCTCTCCTGCCCGGGTGG 2280
      +-----+-----+-----+-----+-----+
      TGTGGTACGACCCGTAGACCTGGGAGGATGGAGACCAC TAGGGAGAGGACGGGCCACCC

2281 AGGCTTACCCCGTCTTAGTCCCGGGGATAGGCAAGTGGGGCGGGCGGGGACGCGTGCG 2340
      +-----+-----+-----+-----+-----+
      TCCGAATGGGGCAGAATCAGGGGCCCTATCCGTTTCAACCCGCGCGCCCTGCGCACGC

2341 GGATTGCGGGCGCAGCGGGCACGCGGGCACCTGGGAGCGGCGGGCTGCTGCGGGAGGGG 2400
      +-----+-----+-----+-----+-----+
      CCTAACGCGCGCGTGGCGCGTGGCCCGTGGACCCTGCGCGCCGACGACGCCCTCCGC

2401 TTGGAGACTGGCTCCCGGGGCTGTTAGGACCTTCCCTCAGGCCCGGGTGTCTCAGAACGA 2460
      +-----+-----+-----+-----+-----+
      AACCTCTGACCGAGGGCCCCGACAATCCTGGAAGGGAGTCCGGGCCACGAGTCTTGCT

2461 TGGAGGACTTGCTTTTCTTGGGCCTTGATGCGAAGTGCTGATCCCGCTGGGCAGGCGGG 2520
      +-----+-----+-----+-----+-----+
      ACCCTCTGAACGAAAAGAACC CGGAAC TACGCTTACGACTAGGGCGACCCGTCCGCCCC

2521 CAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTTGAGGTGGGCGTGGGGGGCGGA 2580
      +-----+-----+-----+-----+-----+
      GTCGAGGCCGCGAGGAGCCTCTGGTGACCGAGGTGCAACTCCACCCGACCCCCCGCCT

2581 CAGGAATTGAAGCGAAGTCTGGGAAGCTTTAGGGTCGCTGGAGGGGGACCCCGGTTGGA 2640
      +-----+-----+-----+-----+-----+
      GTCCCTTAACCTTCGACCTTCAGACCTTCGAAATCCAGCGACCTCCCCCTGGGGCCAACCT

      <---- 4.p53-BE ---->
      (intron)

2641 GAGAGGAGCGGAACTCCTGGACAAGCCCTGACAAGCCAAGCCAAAGGTCCGCTCCGGCGC 2700
      +-----+-----+-----+-----+-----+
      CTCTCCTCGCCTTGAGGACCTGTTCGGGACTGTTCGGTTCGGTTTCCAGGCGAGGCCGCG

```

Fig. 10C

APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	241

2701 GGGTGGGTGAGTGC GCGCCGCCCGCGGGGGGAGAGAGCCTACAGCCTTCAGAACA 2760  
 -----  
 CCCACCCACTCACGCGCGGGCGGGCGCCCCGCCCTCTCTCGGATGTCGGAAGTCTTGT  
 2761 CATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTG 2820  
 -----  
 GTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTTATTTCAGTCGTGGCTTCGTAC  
 2821 GTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTCTCGAAAAGTTATATGGGG 2880  
 -----  
 CAATTGGGCTCCCGAGCCTTCTTGCCGTGGAAAAGAAAGAGCTTTTCAATATACCCC  
 2881 CTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTATTGTACACAGAAAAGGAACTG 2940  
 -----  
 GACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAACAGTGTGTCTTTTCCTTTGAC  
 2941 CCTTGCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTC 3000  
 -----  
 GGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACATTCAGCGACGGACTCACCAAAG  
 3001 ATTTTGTITTTGTTTTCTGCCCTTCTCTTTCTTTTGGCCCTTTCTTAGCTTGCACTCC 3060  
 -----  
 TAAAAAACAACAAAAGACGGGAAGAGAAAGAAACGGGAAGAATCGAACGTGAGG  
 3061 CATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCACCGCACAGA 3120  
 -----  
 GTACCACTAAAGACGAACCAGAGGACGACCCCAACCACCATGAGCAAGGGTGGCGTGTCT  
 3121 ACCCGCGCCTATTATTGGCCAAGAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTC 3180  
 -----  
 TGGGCCGCGGATAATAACCGGTTCTTTGAACTCGTGCGACAAAACTTTCAGGGAGCGAG  
 3181 AGAAATGCCAGCTTGCGATGGCTAATCAAAG 3212  
 -----  
 TCTTTACGGTCGAACGTCTACCGATTAGTTTC

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Fig. 10D

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	S36	24.1

## Fig. 11A

variations in the p53 binding region of figure 8

### 1. p1140 IMI

```

p1140          GGACAAGCCCTGACAAGCCA
p1140 IMI      GGAAAAGCCCTGACAAGCCA
                  ↑
  
```

positions of the mutations (boldface and arrow): 2270 (C→A)

### 2. p1140 IMII

```

p1140          GGACAAGCCCTGACAAGCCA
p1140 IMII      GGAAAAGCCCTGAAAAGCCA
                  ↑      ↑
  
```

positions of the mutations (boldface and arrow): 2270 (C→A)  
2280 (C→A)

### 3. p1140 IMIII

```

p1140          GGACAAGCCCTGACAAGCCA
p1140 IMIII     GGAAAATCCCTGAAAATCCA
                  ↑  ↑      ↑  ↑
  
```

positions of the mutations (boldface and arrow): 2270 (C→A)  
2273 (G→T)  
2280 (C→A)  
2283 (G→T)

FOI 04-01-2004

APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

Fig. 11B

4. p1140 IMIV

p1140

GGACAAGCCCTGACAAGCCA

p1140 IMIV

GCACAAGCCCT**C**ACAAGCCA

↑

↑

positions of the mutations (boldface and arrow): 2268 (G→T)

2278 (C→A)

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APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

## Fig. 12A

variations in the p53 binding regions of figure 9

### 1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GG <b>AAA</b> ATCCCTG <b>AAA</b> ATCCA
	↑ ↑     ↑ ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

### 2. p1141 1p53

p1141	AGAGATGCCCAA <b>ACT</b> GTTTT
p1141 1p53	AGAGAT <b>TCCCAA</b> <b>AAT</b> GTTTT
	↑            ↑

positions of the mutations (boldface and arrow): 50

57

### 3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTTTT
p1141 2p53	AATGTT <b>TCTTAAG</b> ATTTTTT
	↑            ↑

positions of the mutations (boldface and arrow): 443

450

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APPROVED	O. G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

## Fig. 12B

### 4. p1141 3p53

p1141	AAACTACCTAAGAGCTATCT
p1141 3p53	ACAATACCTAAGAGCTATCT
	↑ ↑

positions of the mutations (boldface and arrow): 1268 (A→C)  
1270 (C→A)

### 5. p1141 ΔBgl

	<---- 1.p53-BE ---->
p1141	AATAACCTTTAGAGATGCCCAAAGCTTTTCCCCAGAACA
p1141ΔBgl	AATAACCTTTA-----GATCTCCCCAGAACA

### 6. p1141 ΔSpe

	<---- 2.p53-BE ---->
p1141	CATCTTTGCCAATGTTGCTTAAGCTTTTGGCTACATTT
p1141ΔBgl	CATCTTTGCCA-----CTAGTGGCTACATTT

### 7. p1141 ΔMph

	<---- 3.p53-BE ---->
p1141	AATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAA
p1141ΔBgl	AATTCATGCTATGCA-----TACCGTTCCAA

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APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	536	24.1

## Fig. 13A

variations in the p53 binding region of figure 10

### 1. p1142 TAG

mutation of the positions: 2227 (A→T)  
2228 (T→A)

### 2. p1142 IMIII

p1142	GGACAAGCCCTGACAAGCCA
p1142 IMIII	GG <b>AAAAT</b> CCCTG <b>AAAAT</b> CCA
	↑ ↑            ↑ ↑

positions of the mutations (boldface and arrow): 2662 (C→A)  
2665 (G→T)  
2672 (C→A)  
2675 (G→T)

### 3. p1142 ΔBgl

	<---- 1.p53-BE ---->
p1142	AATAACCTTTAGAGATGCCCCAACTGTTTTCCCCAGAACA
p1142ΔBgl	AATAACCTTTA-----GATCTCCCCAGAACA

### 4. p1142 ΔSpe

	<---- 2.p53-BE ---->
p1142	CATCTTTGCCAATGTTGCTTAAGCTTTTTGGCTACATT
p1142ΔBgl	CATCTTTGCCA-----CTAGTGGCTACATT

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APPROVED	O G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN	534	24.1

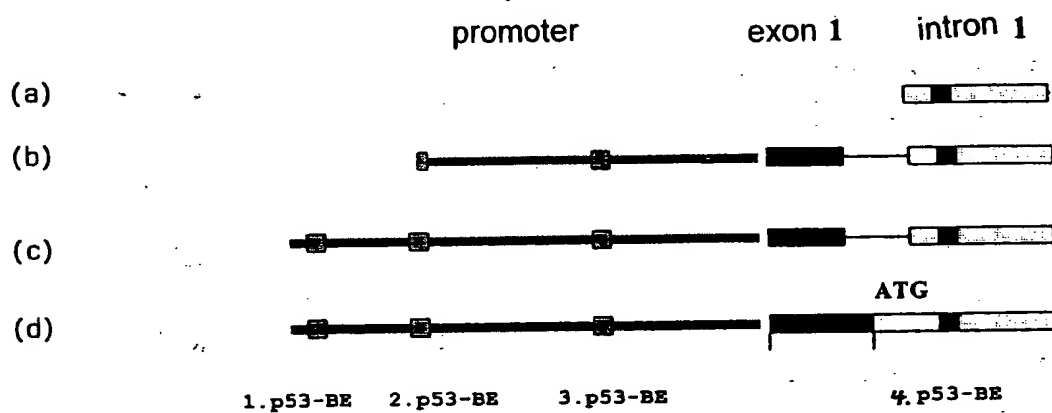


Fig. 14

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